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OM protein - protein search, using sw model

Run on: November 6, 2004, 19:24:00 ; Search time 93.625 Seconds
(without alignments)
43.019 Million cell updates/sec

Title: US-10-618-644-2
Perfect score: 42
Sequence: 1 PNNKPFQ 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 02:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	100.0	328	2 Q8QKT2	Q8qkt2 influenza a
2	42	100.0	328	2 Q8QKT3	Q8qkt3 influenza a
3	42	100.0	328	2 Q8QKT4	Q8qkt4 influenza a
4	42	100.0	328	2 Q8QKT5	Q8qkt5 influenza a
5	42	100.0	328	2 Q8QKT6	Q8qkt6 influenza a
6	42	100.0	328	2 Q8QKT7	Q8qkt7 influenza a
7	42	100.0	328	2 Q8QKT8	Q8qkt8 influenza a
8	42	100.0	363	2 Q6DM43	Q6dm43 influenza a
9	42	100.0	363	2 Q6DM28	Q6dm28 influenza a
10	42	100.0	481	1 GLC3_SOYBN	P11828 glycine max
11	42	100.0	481	2 Q852U5	Q852u5 glycine max
12	42	100.0	482	2 Q852U4	Q852u4 glycine max
13	42	100.0	485	1 GLC2_SOYBN	P04405 glycine max
14	42	100.0	485	2 BAC78523	Bac78523 glycine m
15	42	100.0	495	1 GLC1_SOYBN	P04776 glycine max
16	42	100.0	495	2 BAC78522	Bac78522 glycine m
17	42	100.0	565	1 HEMA_IAHUR	P17002 influenza a
18	39	92.9	328	2 Q8QKT9	Q8qkt9 influenza a
19	37	88.1	211	2 Q8V6Y6	Q8v6y6 influenza a
20	37	88.1	236	2 Q786K6	Q786k6 influenza a
21	37	88.1	236	2 Q786K7	Q786k7 influenza a
22	37	88.1	236	2 Q786L2	Q786l2 influenza a
23	37	88.1	236	2 Q786L3	Q786l3 influenza a
24	37	88.1	236	2 Q9W8J7	Q9w8j7 influenza a
25	37	88.1	236	2 Q9W821	Q9w821 influenza a
26	37	88.1	281	2 Q7TCQ6	Q7tcq6 influenza a
27	37	88.1	281	2 Q7TCQ8	Q7tcq8 influenza a
28	37	88.1	281	2 Q7TCR5	Q7tcr5 influenza a
29	37	88.1	281	2 Q7TCR0	Q7tcr0 influenza a
30	37	88.1	281	2 Q7TCT4	Q7tct4 influenza a
31	37	88.1	281	2 Q91LS8	Q91ls8 influenza a

32 37 88.1 281 2 Q91LT2 Q91lt2 influenza a
33 37 88.1 281 2 Q91LT4 Q91lt4 influenza a
34 37 88.1 281 2 Q91LT5 Q91lt5 influenza a
35 37 88.1 281 2 Q91LT6 Q91lt6 influenza a
36 37 88.1 281 2 Q91LT7 Q91lt7 influenza a
37 37 88.1 281 2 Q91LT8 Q91lt8 influenza a
38 37 88.1 281 2 Q91LT9 Q91lt9 influenza a
39 37 88.1 281 2 Q91LU0 Q91lu0 influenza a
40 37 88.1 281 2 Q91LU1 Q91lu1 influenza a
41 37 88.1 281 2 Q91LU3 Q91lu3 influenza a
42 37 88.1 286 2 Q77QA8 Q77qa8 influenza a
43 37 88.1 286 2 Q77QA9 Q77qa9 influenza a
44 37 88.1 286 2 Q77QB0 Q77qb0 influenza a
45 37 88.1 286 2 Q77QB1 Q77qb1 influenza a

ALIGNMENTS

RESULT 1
Q8QKT2 PRELIMINARY; PRT; 328 AA.
AC Q8QKT2;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Hemagglutinin (Fragment)
OS Influenza A virus (A/Finland/665/99(H3N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H3N2 subtype.
ON NCBI_TaxID=185997;
RX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2250278; PubMed=12403110;
RA Pynaia R., Ikonen N., Haanpaa M., Santanen R., Tervahauta R.;
RT "Phylogenetic and antigenic analysis of influenza A(H3N2) viruses
isolated from conscripts receiving influenza vaccine prior to the
epidemic season of 1998/9.";
RT Epidemiol. Infect. 129:347-353(2002).
CC -I- FUNCTION: Hemagglutinin is responsible for attaching the virus to
cell receptors and for initiating infection (By similarity).
CC -I- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains
(HA1 and HA2) linked by a disulfide bond (By similarity).
CC -I- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
DR EMBL: AF442466; AAL77312.1; -
DR GO: GO:0019031; C:Viral envelope; IEA.
DR GO: GO:0019058; P:Viral infectious cycle; IEA.
DR InterPro: IPR008980; Capsid hemag.
DR InterPro: IPR001364; Hemagglutn.
DR InterPro: IPR000149; Hemagglutn.1.
DR Pfam: PF00509; Hemagglutinin; 1.
DR PRINTS: PR00330; HEMAGGLUTN1.
DR PRINTS: PR00329; HEMAGGLUTN1.
DR ProDom: PD000225; Hemagglutn.1.
KW Envelope protein; Glycoprotein; Hemagglutinin.
FT NON_TER 1
FT NON_TER 328 328
SQ SEQUENCE 328 AA; 36350 MW; DD69D8501D8B5C55 CRC64;

Query Match 100.0%; Score 42; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNNKPFQ 7
Db 289 PNNKPFQ 295

RESULT 2
Q8QKT3 PRELIMINARY; PRT; 328 AA.
ID Q8QKT3
AC Q8QKT3;
DT 01-JUN-2002 (Tremblrel. 21, Created)

01-JUN-2002 (Tremblrel. 21, Last sequence update)
01-MAR-2004 (Tremblrel. 26, Last annotation update)
Hemagglutinin (Fragment).
Influenza A virus (A/Finland/659/99 (H3N2)).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A; H3N2 subtype.
NCBI_TaxID=185996;
[1]
SEQUENCE FROM N.A.
MEDLINE=22290278; PubMed=12403110;
Pyhala R., Ikonen N., Haanpaa M., Santanen R., Tervahauta R.;
"Phylogenetic and antigenic analysis of influenza A(H3N2) viruses
isolated from conscripts receiving influenza vaccine prior to the
epidemic season of 1998/9";
Epidemiol. Infect. 129:347-353(2002).
CC -!- FUNCTION: Hemagglutinin is responsible for attaching the virus to
cell receptors and for initiating infection (By similarity).
CC -!- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains
(HA1 and HA2) linked by a disulfide bond (By similarity).
CC -!- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
EMBL; AF442465; AAL77311.1; -.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019058; P:viral infectious cycle; IEA.
InterPro; IPR008980; Capsid hemag.
InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; 1.
PRINTS; PR00330; HEMAGGLUTN1.
PRODOM; PD000225; Hemagglutn; 1.
Envelope protein; Glycoprotein; Hemagglutinin.
NON_TER 1
FT NON_TER 328 328
FT NON_TER 328 AA; 36224 MW; 88AD94DAB14F35B CRC64;
SEQUENCE 328 AA; 36224 MW; 88AD94DAB14F35B CRC64;
Query Match 100.0%; Score 42; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 6.7; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;
QY 1 PNNKPFQ 7
DB 289 PNNKPFQ 295
RESULT 3
Q8QKT4 PRELIMINARY; PRT; 328 AA.
AC Q8QKT4
ID Q8QKT4
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Hemagglutinin (Fragment).
OS Influenza A virus (A/Finland/684/99 (H3N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H3N2 subtype.
NCBI_TaxID=185995;
[1]
SEQUENCE FROM N.A.
MEDLINE=22290278; PubMed=12403110;
Pyhala R., Ikonen N., Haanpaa M., Santanen R., Tervahauta R.;
"Phylogenetic and antigenic analysis of influenza A(H3N2) viruses
isolated from conscripts receiving influenza vaccine prior to the
epidemic season of 1998/9";
Epidemiol. Infect. 129:347-353(2002).
CC -!- FUNCTION: Hemagglutinin is responsible for attaching the virus to
cell receptors and for initiating infection (By similarity).
CC -!- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains
(HA1 and HA2) linked by a disulfide bond (By similarity).
CC -!- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
EMBL; AF442464; AAL77310.1; -.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019058; P:viral infectious cycle; IEA.
InterPro; IPR008980; Capsid hemag.
InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; 1.
PRINTS; PR00330; HEMAGGLUTN1.
PRODOM; PD000225; Hemagglutn; 1.
Envelope protein; Glycoprotein; Hemagglutinin.
NON_TER 1
FT NON_TER 328 328
FT NON_TER 328 AA; 36224 MW; 88AD94DAB14F35B CRC64;
SEQUENCE 328 AA; 36224 MW; 88AD94DAB14F35B CRC64;
Query Match 100.0%; Score 42; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 6.7; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;
QY 1 PNNKPFQ 7
DB 289 PNNKPFQ 295
RESULT 3
Q8QKT4 PRELIMINARY; PRT; 328 AA.
AC Q8QKT4
ID Q8QKT4
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Hemagglutinin (Fragment).
OS Influenza A virus (A/Finland/684/99 (H3N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H3N2 subtype.
NCBI_TaxID=185995;
[1]
SEQUENCE FROM N.A.
MEDLINE=22290278; PubMed=12403110;
Pyhala R., Ikonen N., Haanpaa M., Santanen R., Tervahauta R.;
"Phylogenetic and antigenic analysis of influenza A(H3N2) viruses
isolated from conscripts receiving influenza vaccine prior to the
epidemic season of 1998/9";
Epidemiol. Infect. 129:347-353(2002).
CC -!- FUNCTION: Hemagglutinin is responsible for attaching the virus to
cell receptors and for initiating infection (By similarity).
CC -!- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains
(HA1 and HA2) linked by a disulfide bond (By similarity).
CC -!- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
EMBL; AF442464; AAL77310.1; -.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019058; P:viral infectious cycle; IEA.
InterPro; IPR008980; Capsid hemag.
InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; 1.
PRINTS; PR00330; HEMAGGLUTN1.
PRODOM; PD000225; Hemagglutn; 1.
Envelope protein; Glycoprotein; Hemagglutinin.
NON_TER 1
FT NON_TER 328 328
FT NON_TER 328 AA; 36224 MW; 88AD94DAB14F35B CRC64;
SEQUENCE 328 AA; 36224 MW; 88AD94DAB14F35B CRC64;
Query Match 100.0%; Score 42; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 6.7; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;
QY 1 PNNKPFQ 7
DB 289 PNNKPFQ 295
RESULT 3
Q8QKT4 PRELIMINARY; PRT; 328 AA.
AC Q8QKT4
ID Q8QKT4
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Hemagglutinin (Fragment).
OS Influenza A virus (A/Finland/684/99 (H3N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H3N2 subtype.
NCBI_TaxID=185995;
[1]
SEQUENCE FROM N.A.
MEDLINE=22290278; PubMed=12403110;
Pyhala R., Ikonen N., Haanpaa M., Santanen R., Tervahauta R.;
"Phylogenetic and antigenic analysis of influenza A(H3N2) viruses
isolated from conscripts receiving influenza vaccine prior to the
epidemic season of 1998/9";
Epidemiol. Infect. 129:347-353(2002).
CC -!- FUNCTION: Hemagglutinin is responsible for attaching the virus to
cell receptors and for initiating infection (By similarity).
CC -!- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains
(HA1 and HA2) linked by a disulfide bond (By similarity).
CC -!- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
EMBL; AF442464; AAL77310.1; -.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019058; P:viral infectious cycle; IEA.
InterPro; IPR008980; Capsid hemag.
InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; 1.
PRINTS; PR00330; HEMAGGLUTN1.
PRODOM; PD000225; Hemagglutn; 1.
Envelope protein; Glycoprotein; Hemagglutinin.
NON_TER 1
FT NON_TER 328 328
FT NON_TER 328 AA; 36224 MW; 88AD94DAB14F35B CRC64;
SEQUENCE 328 AA; 36224 MW; 88AD94DAB14F35B CRC64;
Query Match 100.0%; Score 42; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 6.7; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;
QY 1 PNNKPFQ 7
DB 289 PNNKPFQ 295
RESULT 3
Q8QKT4 PRELIMINARY; PRT; 328 AA.
AC Q8QKT4
ID Q8QKT4
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Hemagglutinin (Fragment).
OS Influenza A virus (A/Finland/684/99 (H3N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H3N2 subtype.
NCBI_TaxID=185995;
[1]
SEQUENCE FROM N.A.
MEDLINE=22290278; PubMed=12403110;
Pyhala R., Ikonen N., Haanpaa M., Santanen R., Tervahauta R.;
"Phylogenetic and antigenic analysis of influenza A(H3N2) viruses
isolated from conscripts receiving influenza vaccine prior to the
epidemic season of 1998/9";
Epidemiol. Infect. 129:347-353(2002).
CC -!- FUNCTION: Hemagglutinin is responsible for attaching the virus to
cell receptors and for initiating infection (By similarity).
CC -!- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains
(HA1 and HA2) linked by a disulfide bond (By similarity).
CC -!- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
EMBL; AF442464; AAL77310.1; -.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019058; P:viral infectious cycle; IEA.
InterPro; IPR008980; Capsid hemag.
InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; 1.
PRINTS; PR

DT 01-JUN-2002 (T-EMBLrel. 21, Created)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Hemagglutinin (Fragment).
 OS Influenza A virus (A/Finland/657/99 (H3N2)).
 OC Viruses; sRNA negative-strand viruses; Orthomyxoviridae;
 OX Influenzavirus A; H3N2 subtype.
 OX NCBI_TaxID=185993;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2290278; PubMed=12403110;
 RA Pyhala R., Ikonen N., Haanpaa M., Santanen R., Tervahauta R.;
 RT "Phylogenetic and antigenic analysis of influenza A(H3N2) viruses
 RT isolated from conscripts receiving influenza vaccine prior to the
 RT epidemic season of 1998/9".
 RL Epidemiol. Infect. 129:347-353(2002).
 CC -1- FUNCTION: Hemagglutinin is responsible for attaching the virus to
 CC cell receptors and for initiating infection (By similarity).
 CC -1- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains
 CC (HA1 and HA2) linked by a disulfide bond (By similarity).
 CC -1- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
 DR EMBL; AF442462; AAL77308.1; -.
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0019058; P:Viral infectious cycle; IEA.
 DR InterPro; IPR008980; Capsid hemag.
 DR InterPro; IPR001364; Hemagglutn.
 DR InterPro; IPR000149; Hemagglutn_1.
 DR Pfam; PF00509; Hemagglutinin; 1.
 DR PRINTS; PR00330; Hemagglutn.1.
 DR PRINTS; PR00329; HEMAGGLUTN12.
 DR ProDom; PD000225; Hemagglutn; 1.
 KW Envelope protein; Glycoprotein; Hemagglutinin.
 FT NON_TER 1 328
 FT SEQUENCE 328 AA; 36254 MW; D014B994DAA8A93F7 CRC64;
 SQ

 Query Match 100.0%; Score 42; DB 2; Length 328;
 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 PNNKPFQ 7
 Db 289 PNNKPFQ 295
 |||||

 RESULT 6
 Q8OKT7
 ID Q8OKT7 PRELIMINARY; PRT; 328 AA.
 AC Q8OKT7;
 DT 01-JUN-2002 (T-EMBLrel. 21, Created)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Hemagglutinin (Fragment).
 OS Influenza A virus (A/Finland/664/99 (H3N2)).
 OC Viruses; sRNA negative-strand viruses; Orthomyxoviridae;
 OX Influenzavirus A; H3N2 subtype.
 OX NCBI_TaxID=185992;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2290278; PubMed=12403110;
 RA Pyhala R., Ikonen N., Haanpaa M., Santanen R., Tervahauta R.;
 RT "Phylogenetic and antigenic analysis of influenza A(H3N2) viruses
 RT isolated from conscripts receiving influenza vaccine prior to the
 RT epidemic season of 1998/9".
 RL Epidemiol. Infect. 129:347-353(2002).
 CC -1- FUNCTION: Hemagglutinin is responsible for attaching the virus to
 CC cell receptors and for initiating infection (By similarity).
 CC -1- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains
 CC (HA1 and HA2) linked by a disulfide bond (By similarity).
 CC -1- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
 DR EMBL; AF442461; AAL77307.1; -.
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0019058; P:Viral infectious cycle; IEA.

DR InterPro; IPR008980; Capsid hemag.
 DR InterPro; IPR001364; Hemagglutn.
 DR InterPro; IPR000149; Hemagglutn_1.
 DR Pfam; PF00509; Hemagglutinin; 1.
 DR PRINTS; PR00330; HEMAGGLUTN1.
 DR PRINTS; PR00329; HEMAGGLUTN12.
 DR ProDom; PD000225; Hemagglutn; 1.
 KW Envelope protein; Glycoprotein; Hemagglutinin.
 FT NON_TER 1 328
 FT SEQUENCE 328 AA; 36327 MW; CADFC850113D4904 CRC64;
 SQ

 Query Match 100.0%; Score 42; DB 2; Length 328;
 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 PNNKPFQ 7
 Db 289 PNNKPFQ 295
 |||||

 RESULT 7
 Q8OKT8
 ID Q8OKT8 PRELIMINARY; PRT; 328 AA.
 AC Q8OKT8;
 DT 01-JUN-2002 (T-EMBLrel. 21, Created)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Hemagglutinin (Fragment).
 OS Influenza A virus (A/Finland/656/99 (H3N2)).
 OC Viruses; sRNA negative-strand viruses; Orthomyxoviridae;
 OX Influenzavirus A; H3N2 subtype.
 OX NCBI_TaxID=185991;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2290278; PubMed=12403110;
 RA Pyhala R., Ikonen N., Haanpaa M., Santanen R., Tervahauta R.;
 RT "Phylogenetic and antigenic analysis of influenza A(H3N2) viruses
 RT isolated from conscripts receiving influenza vaccine prior to the
 RT epidemic season of 1998/9".
 RL Epidemiol. Infect. 129:347-353(2002).
 CC -1- FUNCTION: Hemagglutinin is responsible for attaching the virus to
 CC cell receptors and for initiating infection (By similarity).
 CC -1- SUBUNIT: Homotrimer. Each of the monomers is formed by two chains
 CC (HA1 and HA2) linked by a disulfide bond (By similarity).
 CC -1- SIMILARITY: Belongs to the influenza viruses hemagglutinin family.
 DR EMBL; AF442460; AAL77306.1; -.
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0019058; P:Viral infectious cycle; IEA.
 DR InterPro; IPR008980; Capsid hemag.
 DR InterPro; IPR001364; Hemagglutn.
 DR InterPro; IPR000149; Hemagglutn_1.
 DR Pfam; PF00509; Hemagglutinin; 1.
 DR PRINTS; PR00330; HEMAGGLUTN1.
 DR PRINTS; PR00329; HEMAGGLUTN12.
 DR ProDom; PD000225; Hemagglutn; 1.
 KW Envelope protein; Glycoprotein; Hemagglutinin.
 FT NON_TER 1 328
 FT SEQUENCE 328 AA; 36281 MW; 40FF4A5E11D347E4 CRC64;
 SQ

 Query Match 100.0%; Score 42; DB 2; Length 328;
 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 PNNKPFQ 7
 Db 289 PNNKPFQ 295
 |||||

 RESULT 8
 Q6DM43
 ID Q6DM43 PRELIMINARY; PRT; 363 AA.

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AC Q6DM43;
DT 01-OCT-2004 (TrEMBLrel. 28, Created)
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hemagglutinin (Fragment).
OS Influenza A virus (A/Lyon/1803/93 (H3N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H3N2 subtype.
OX NCBI_TaxID=282947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/Lyon/1803/93;
RA Smith D.J., Lapedes A.S., de Jong J.C., Bestebroer T.M.,
RA Osterhaus A.D.M.E., Fouchier R.A.M.;
RT "Mapping the Antigenic and Genetic Evolution of Influenza Virus.";
RL Science 0:0-0(2004).
DR EMBL; AY661169; ANT64844.1; -.
FT NON_TER 363
SQ SEQUENCE 363 AA; 40073 MW; 17B27B34A8AC034C CRC64;

Query Match 100.0%; Score 42; DB 2; Length 363;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNNKPFQ 7
Db 305 PNNKPFQ 311

RESULT 9
Q6DM8 PRELIMINARY; PRT; 363 AA.
ID Q6DM8;
AC Q6DM8;
DT 01-OCT-2004 (TrEMBLrel. 28, Created)
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hemagglutinin (Fragment).
OS Influenza A virus (A/Singapore/53/89 (H3N2)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H3N2 subtype.
OX NCBI_TaxID=282858;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/Singapore/53/89;
RA Smith D.J., Lapedes A.S., de Jong J.C., Bestebroer T.M.,
RA Osterhaus A.D.M.E., Fouchier R.A.M.;
RT "Mapping the Antigenic and Genetic Evolution of Influenza Virus.";
RL Science 0:0-0(2004).
DR EMBL; AY661064; ANT64739.1; -.
FT NON_TER 363
SQ SEQUENCE 363 AA; 40181 MW; B666EDB15E94BA86 CRC64;

Query Match 100.0%; Score 42; DB 2; Length 363;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNNKPFQ 7
Db 305 PNNKPFQ 311

RESULT 10
GLC3 SOYBN STANDARD; PRT; 481 AA.
ID GLC3 SOYBN
AC P11828;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Glycinin G3 precursor [Contains: Glycinin A subunit; Glycinin B subunit].
DE subunit.
OS Glycine max (Soybean).
GN Name=GY3;
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
NCBI_TaxID=3847;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Dare; TISSUE=Leaf;
MEDLINE=89296500; PubMed=2740231;
Cho T.-J., Nielsen N.C.;
"The glycinin G3 gene from soybean.";
Nucleic Acids Res. 17:4388-4388(1989).
[2]
DISCUSSION OF SEQUENCE.
MEDLINE=92393391; PubMed=2485233;
Nielsen N.C., Dickinson C.D., Cho T.-J., Thanh V.H., Scallan B.J.,
Fischer R.L., Sims T.L., Drews G.N., Goldberg R.B.;
"Characterization of the glycinin gene family in soybean.";
Plant Cell 1:313-328(1989).
-!- FUNCTION: Glycinin is the major seed storage protein of soybean.
-!- SUBUNIT: Hexamer; each subunit is composed of an acidic and a
basic chain derived from a single precursor and linked by a
disulfide bond.
-!- SIMILARITY: Belongs to the 11S seed storage protein (globulins)
family.
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EMBL; X15123; CAA33217.1; -.
PIR; S04605; S04605.
HSP; P04776; IFXZ.
InterPro; IPR006045; Cupin.
InterPro; IPR007113; Cupin region.
InterPro; IPR011051; RmlC like cupin.
InterPro; IPR006044; Seedstore_11s.
Pfam; PF00190; Cupin; 2.
PRINTS; PR00439; 11SGLOBULIN.
PROSITE; PS00305; 11S_SEED_STORAGE; 1.
KW Multigene family; Seed storage protein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 296 Glycinin A subunit.
FT CHAIN 297 476 Glycinin B subunit.
FT PROPEP 477 481
FT DISULFID 107 303 Interchain (By similarity).
SQ SEQUENCE 481 AA; 54241 MW; 5F3C3148DF6241A7 CRC64;

Query Match 100.0%; Score 42; DB 1; Length 481;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNNKPFQ 7
Db 57 PNNKPFQ 63

RESULT 11
Q852U5 PRELIMINARY; PRT; 481 AA.
ID Q852U5
AC Q852U5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Glycinin AlbB2-445.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
NCBI_TaxID=3847;
[1]

```

RP SEQUENCE FROM N.A.
 RC STRAIN=Matsuura; TISSUE=Seed;
 RA Fukazawa C.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBUNIT: Hexamer; each subunit is composed of an acidic and a
 CC basic chain derived from a single precursor and linked by a
 CC disulfide bond (By similarity).
 CC -1- SIMILARITY: Belongs to the 11S seed storage protein (globulins)
 CC family.
 CC EMBL; AB030494; BAC55937.1; -.
 DR HSSP; P04776; IPXZ.
 DR GO; GO:0045735; P:nutrient reservoir activity; IEA.
 DR InterPro; IPR006045; Cupin.
 DR InterPro; IPR007113; Cupin region.
 DR InterPro; IPR011051; Rn1C like cupin.
 DR InterPro; IPR006044; Seedstore_11s.
 DR Pfam; PF00190; Cupin; 2.
 DR PRINTS; PR00439; IISGLOBULIN.
 DR PROSITE; PS00305; 11S SEED STORAGE; 1.
 DR Seed storage protein; Storage protein.
 KW SEQUENCE 481 AA; 54217 MW; 4F4853F27C98BE69B CRC64;
 SQ

Query Match 100.0%; Score 42; DB 2; Length 481;

Best Local Similarity 100.0%; Pred. No. 9.9;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNNKPFQ 7

Db 57 PNNKPFQ 63

RESULT 12

Q852U4 ID Q852U4 PRELIMINARY; PRT; 482 AA.
 AC Q852U4;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Glycinin A1B2-784.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OC NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Matsuura; TISSUE=Seed;
 RA Fukazawa C.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB030495; BAC55938.1; -.
 DR HSSP; P04776; IPXZ.
 DR GO; GO:0045735; P:nutrient reservoir activity; IEA.
 DR InterPro; IPR006045; Cupin.
 DR InterPro; IPR007113; Cupin region.
 DR InterPro; IPR011051; Rn1C like cupin.
 DR InterPro; IPR006044; Seedstore_11s.
 DR Pfam; PF00190; Cupin; 2.
 DR PRINTS; PR00439; IISGLOBULIN.
 DR PROSITE; PS00305; 11S SEED STORAGE; UNKNOWN 1.
 DR Seed storage protein; Storage protein.
 KW SEQUENCE 482 AA; 54298 MW; 79086863D946BCD CRC64;
 SQ

Query Match 100.0%; Score 42; DB 2; Length 482;

Best Local Similarity 100.0%; Pred. No. 10;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNNKPFQ 7

Db 57 PNNKPFQ 63

RESULT 13

GLC2_SOYBN ID GLC2_SOYBN STANDARD; PRT; 485 AA.
 AC GLC2_SOYBN;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Glycinin A2B1a.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OC NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Matsuura; TISSUE=Seed;
 RA Fukazawa C.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB030496; BAC55939.1; -.
 DR HSSP; P04777; IPXZ.
 DR GO; GO:0045735; P:nutrient reservoir activity; IEA.
 DR InterPro; IPR006045; Cupin.
 DR InterPro; IPR007113; Cupin region.
 DR InterPro; IPR011051; Rn1C like cupin.
 DR InterPro; IPR006044; Seedstore_11s.
 DR Pfam; PF00190; Cupin; 2.
 DR PRINTS; PR00439; IISGLOBULIN.
 DR PROSITE; PS00305; 11S SEED STORAGE; UNKNOWN 1.
 DR Seed storage protein; Storage protein.
 KW SEQUENCE 482 AA; 54298 MW; 79086863D946BCD CRC64;
 SQ

AC P04405; P04121; P04348; P04349;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Glycinin G2 precursor [Contains: Glycinin A2 subunit; Glycinin B1a subunit].
 DE subunit1.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OC NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Dars; TISSUE=Leaf;
 RX MEDLINE=92333391; PubMed=2485233;
 RA Nielsen N.C.; Dickinson C.D.; Cho T.J.; Thanh V.H.; Scallan B.J.;
 RA Fischer R.L.; Sims T.L.; Drews G.N.; Goldberg R.B.;
 RT "Characterization of the glycinin gene family in soybean."
 RL Plant Cell 1:313-328(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Dars; TISSUE=Leaf;
 RX MEDLINE=89296499; PubMed=2740230;
 RA Thanh V.H.; Turner N.E.; Nielsen N.C.;
 RT "The glycinin Gy2 gene from soybean."
 RL Nucleic Acids Res. 17:4387-4387(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Shiroteaurunoko;
 RA Utsunomiya S.; Kim C.S.; Kohno M.; Kito M.;
 RT "Polymorphism and expression of cDNAs encoding glycinin subunits."
 RL Agric. Biol. Chem. 51:3267-3273(1987).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=88040439; PubMed=3671077;
 RA Fukazawa C.; Momma T.; Higuchi W.; Uda K.;
 RT "Complete nucleotide sequence of the gene encoding a glycinin A2B1a subunit precursor of soybean."
 RL Nucleic Acids Res. 15:8117-8117(1987).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Momma T.; Negoro T.; Uda K.; Fukazawa C.;
 RT "A complete cDNA coding for the sequence of glycinin A2B1a subunit precursor."
 RL FEBS Lett. 188:117-122(1985).
 RN [6]
 RP SEQUENCE OF 19-296 AND 301-480 (A2 AND B1a SUBUNITS).
 RX MEDLINE=85030470; PubMed=6541652;
 RA Staswick P.E.; Hermodson M.A.; Nielsen N.C.;
 RT "The amino acid sequence of the A2B1a subunit of glycinin."
 RL J. Biol. Chem. 259:13424-13430(1984).
 RN [7]
 RP SEQUENCE OF 262-485 FROM N.A.
 RX MEDLINE=85030472; PubMed=6092376;
 RA Marco Y.A.; Thanh V.H.; Turner N.E.; Scallan B.J.; Nielsen N.C.;
 RT "Cloning and structural analysis of DNA encoding an A2B1a subunit of glycinin."
 RL J. Biol. Chem. 259:13436-13441(1984).
 RN [8]
 RP SEQUENCE OF 1-36 FROM N.A.
 RX MEDLINE=90332420; PubMed=2377465;
 RA Kitamura Y.; Arahira M.; Itoh Y.; Fukazawa C.;
 RT "The complete nucleotide sequence of soybean glycinin A2B1a gene spanning to another glycinin gene AlaB1b."
 RL Nucleic Acids Res. 18:4245-4245(1990).
 RN [9]
 RP DISULFIDE BOND.
 RX MEDLINE=85030471; PubMed=6541653;
 RA Staswick P.E.; Hermodson M.A.; Nielsen N.C.;
 RT "Identification of the cysteines which link the acidic and basic components of the glycinin subunits."
 RL J. Biol. Chem. 259:13431-13435(1984).

CC -!- FUNCTION: Glycinin is the major seed storage protein of soybean.
CC -!- SUBUNIT: Hexamer; each subunit is composed of an acidic and a
CC basic chain derived from a single precursor and linked by a
CC disulfide bond.
CC -!- SIMILARITY: Belongs to the 11S seed storage protein (globulins)
CC family.
CC -----
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CC -----

DR EMBL; X15122; CAA33216.1; -;
DR EMBL; D00216; BAA00154.1; -;
DR EMBL; Y00398; CAA68460.1; -;
DR EMBL; X02806; CAA36575.1; -;
DR EMBL; K02646; AAA33963.1; -;
DR EMBL; X53404; CAA37480.1; -;
DR PIR; A91341; FWSYGL.
DR PIR; S11002; S11002.
DR HSSP; P04776; 1FXZ.
DR InterPro; IPR006045; Cupin.
DR InterPro; IPR011051; RmlC like cupin.
DR Pfam; PF00190; Cupin; 2.
DR PRINTS; PR00439; 11SGLOBULIN.
DR PROSITE; PS00305; 11S SEED STORAGE; 1.
KW Direct protein sequencing; Multigene family; Seed storage protein;
KW Signal.
FT SIGNAL 1 18
FT CHAIN 19 296 Glycinin A2 subunit.
FT PROPEP 297 300
FT CHAIN 301 480 Glycinin B1A subunit.
FT PROPEP 481 485
FT DISULFID 104 307 Interchain.
FT VARIANT 103 103 G -> D.
FT VARIANT 318 318 N -> T.
FT VARIANT 331 331 I -> V.
FT VARIANT 413 413 K -> R.
FT CONFLICT 39 39 D -> N (in Ref. 6).
FT CONFLICT 39 39 D -> G (in Ref. 5).
FT CONFLICT 61 61 C -> S (in Ref. 6).
FT CONFLICT 117 117 R -> C (in Ref. 6).
FT CONFLICT 343 343 W -> S (in Ref. 6).
SQ SEQUENCE 485 AA; 54391 MW; 78BB459837F77AD8 CRC64;

Query Match 100.0%; Score 42; DB 1; Length 485;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PNNKPFQ 7
Db 54 PNNKPFQ 60
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RESULT 14
BAC78523 PRELIMINARY; PRT; 485 AA.
AC BAC78523;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE Proglycinin A2B1.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.

RA Urade R., Nakatani H.;
RT "mRNA of Soybean Proglycinin A2B1 Subunit."
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB113350; BAC78523.1; -;
SQ SEQUENCE 485 AA; 54390 MW; 78BB459837F77AD8 CRC64;
Query Match 100.0%; Score 42; DB 2; Length 485;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PNNKPFQ 7
Db 54 PNNKPFQ 60
|||||

RESULT 15
GLC1 SOYBN
ID GLC1 SOYBN STANDARD; PRT; 495 AA.
AC P04776;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Glycinin G1 precursor [Contains: Glycinin A1A subunit; Glycinin Bx
DE subunit].
GN Name=GY1;
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Dare; TISSUE=Leaf;
RX MEDLINE=92393391; PubMed=2485233;
RA Nielsen N.C., Dickinson C.D., Cho T.J., Thanh V.H., Scallan B.J.,
RA Fischer R.L., Sims T.L., Drews G.N., Goldberg R.B.;
RT "Characterization of the glycinin gene family in soybean."
RL Plant Cell 1:313-328(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Dare; TISSUE=Leaf;
RX MEDLINE=89296498; PubMed=2740229;
RA Sims T.L., Goldberg R.B.;
RT "The glycinin G1 gene from soybean."
RL Nucleic Acids Res. 17:4386-4386(1989).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Bonminori;
RX MEDLINE=86041867; PubMed=2997720;
RA Negoro T., Momma T., Fukazawa C.;
RT "A cDNA clone encoding a glycinin Ala subunit precursor of soybean."
RL Nucleic Acids Res. 13:6719-6731(1985).
RN [4]
RP SEQUENCE FROM N.A.
RA Utsumi S., Kohno M., Mori T., Kito M.;
RT "An alternate cDNA encoding glycinin Ala Bx subunit."
RL J. Agric. Food Chem. 35:210-214(1987).
RN [5]
RP SEQUENCE FROM N.A.
RA Urade R., Nakatani H., Nakano C.;
RT "mRNA of soybean proglycinin A1A1b subunit."
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Glycinin is the major seed storage protein of soybean.
CC -!- SUBUNIT: Hexamer; each subunit is composed of an acidic and a
CC basic chain derived from a single precursor and linked by a
CC disulfide bond.
CC -!- PTM: The precursor is post-translational processed to form a
CC covalently linked A1A-Bx subunit complex.
CC -!- SIMILARITY: Belongs to the 11S seed storage protein (globulins)
CC family.
CC -----
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DR EMBL; M36686; AAA33966.1; --
DR EMBL; X15121; CAA33215.1; --
DR EMBL; X02985; CAA26723.1; --
DR EMBL; AB113349; BAC78522.1; --
DR PIR; A23497; FWSYG2.
DR PIR; S10851; S10851.
DR PDB; 1FX2; X-ray; A/B/C=20-495.
DR PDB; 1UCX; X-ray; A/B/C=20-495.
DR PDB; 1UDI; X-ray; A/B/C=20-495.
DR InterPro; IPR006045; Cupin.
DR InterPro; IPR007113; Cupin region.
DR InterPro; IPR011051; RmlC like cupin.
DR InterPro; IPR006044; Seedstore_11s.
DR Pfam; PF00190; Cupin; 2.
DR PRINTS; PR00439; IISGLOBULIN.
DR PROSITE; PS00305; IIS_SEED_STORAGE; 1.
KW 3D-structure; Multigene family; Seed storage protein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 306 Glycinin A1A subunit.
FT PROPEP 307 310 Glycinin BX subunit.
FT CHAIN 311 490
FT PROPEP 491 495
FT DISULFID 107 317 Interchain (By similarity).
FT CONFLICT 42 42 D -> G (in Ref. 3).
FT CONFLICT 108 108 P -> S (in Ref. 3).
FT CONFLICT 136 136 E -> S (in Ref. 3).
FT CONFLICT 360 360 E -> G (in Ref. 3).
FT TURN 30 31
FT STRAND 39 39
FT STRAND 43 47
FT TURN 48 49
FT STRAND 50 54
FT TURN 57 58
FT HELIX 60 65
FT TURN 66 66
FT STRAND 68 74
FT TURN 76 77
FT STRAND 78 84
FT STRAND 89 95
FT TURN 97 103
FT STRAND 105 106
FT TURN 134 137
FT TURN 138 139
FT STRAND 140 144
FT TURN 146 147
FT STRAND 149 154
FT STRAND 160 166
FT TURN 168 169
FT TURN 171 172
FT STRAND 181 183
FT TURN 191 192
FT HELIX 193 196
FT TURN 222 223
FT HELIX 226 233
FT TURN 234 234
FT HELIX 237 243
FT STRAND 255 257
FT TURN 317 318
FT STRAND 322 324
FT STRAND 333 335
FT TURN 336 338
FT STRAND 339 344
FT TURN 346 348
FT HELIX 350 352
FT TURN 353 356
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FT TURN 366 367

FT STRAND 369 375
FT TURN 376 377
FT STRAND 380 386
FT STRAND 388 394
FT TURN 396 397
FT STRAND 400 407
FT TURN 408 409
FT STRAND 411 414
FT TURN 416 417
FT STRAND 419 424
FT TURN 427 428
FT STRAND 429 435
FT STRAND 442 444
FT TURN 448 449
FT TURN 451 451
FT HELIX 452 454
FT HELIX 457 464
FT TURN 465 465
FT HELIX 468 476
FT STRAND 483 484
SQ SEQUENCE 495 AA; 55706 MW; 329CB0545B24D894 CRC64;

Query Match 100.0%; Score 42; DB 1; Length 495;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNNKPFQ 7
Db 57 PNNKPFQ 63

Search completed: November 6, 2004, 19:52:48
Job time : 94.625 secs

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